STUDY OF MICROORGANISMS WITHIN THE HOUSING ENVIRONMENT

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ABSTRACT

Bacteria are found virtually in every environment. High levels of indoor bacteria concentration is an indication of high occupancy rate, poor ventilation, or poor building maintenance. We study airborne Bacteria in Indoor Environments in two residences areas covering summer, winter season to study the climate effect (temperature) also covering high level and low level population to study the quality of life (good aeration, ventilation and variation of occupation area per citizens). We examine the presence of airborne Bacteria in Indoor Environments and colony forming unit for each case and we found that Exiguobacterium sp was the most frequent bacteria (37.5%) in high level population during the Summer climate, Bacillus sp was the most frequent bacteria (26.7%) in high level population during the Winter climate, Brachybacterium sp was the most frequent bacteria (42.4%) during the summer climate and kytococcus sp was the most frequent bacteria (32.2%) in low level population during the winter climate. We found a significant increase in colony forming unit among low level residence population during summer with Minimum, Maximum, Mean value 17.5, 25, 21.69 CFU/m3 respectively than among High level residence population in summer with Minimum, Maximum, Mean value 7.92, 14.58, 10.97 CFU/m3 respectively with p-value <0.001 which indication the negative effect of high occupancy rate, poor ventilation on quality of life and a significant increase in colony forming unit in high level residence population in summer with Minimum, Maximum, Mean value 7.92, 14.58, 10.69 CFU/m3 respectively than in high level residence population in winter with Minimum, Maximum, Mean value 0.42, 2.5, 1.39 CFU/m3 respectively with p-value <0.001 which indicate high level of airborne bacteria due to high temperature .

INTRODUCTION

How safe is the air in your surrounding environment that you spend much of your time? Indoor environments are fundamental environmental factors capable of impacting health. Air quality of indoor environments is one of the main factors affecting health, wellbeing and productivity of people. One of the problems of indoor air quality is affected by the presence of microorganisms which include bacteria, moulds and viruses (Wamedo S *et al*., 2012) People spends 80%- 90% of their time in indoors environments[Awad & Farag 1999] breathing on average 14 m3 of air per day[Brochu *et al*., 1999]. these make people highly exposed to indoor air environments. In recent years there has been a growing interest of indoor microbe studies [WHO 2009]. The activity of people within the indoor environments is thought to be the principal factor contributing to the buildup and spread of airborne microbial contamination [Qian *et al*., 2012]. Particular activities like talking, sneezing, coughing, walking and washing can generate airborne biological particulate matter. A review made by WHO on the number of epidemiological studies showed that there is sufficient evidence for an association between indoor dampness-related factors and a wide range of effects on respiratory health, including asthma development, asthma exacerbation, current asthma, respiratory infections, upper respiratory tract symptoms(cough, wheeze and dyspnea)[WHO 2009]. Thus microbiological air quality is an important criterion that must be taken into account when indoor workplaces are designed to provide a safe environment. This study provides

information on the concentration of microorganisms and describes bacterial loads for different seasonal climate changes. Moreover, the impact of environmental factors (population level variation) on their multiplication and growth in the indoor air.Thus, the microbial loads of the buildings were favored by the environmental conditions which enhance their development. And also it was stated by WHO that dampness situation has to be considered as the risk indicator for health risks of biological contaminants of indoor air [WHO 2009].

AIM OF STUDY

- To identify and classify bacteria in our homes
- To assess the microbiological, indoor air quality (IAQ) in our home
- To evaluate the possible effect of temperature variation on bacterial growth.

MATERIAL AND METHOD

We study airborne Bacteria in Indoor Environments in two groups according to socioeconomic level (low and high), They were studied during summer and winter season to study the climate effect (temperature). High level population represent very spacious newly built & well designed houses.(all residents have high income and social strata) and low level population represent poor houses, each was a single room or more but didn't exceed three room all which were built at random. (These shelters are inhabited by poor low income expatriate population usually more than 3 individuals per room)

To evaluate the concentration of bacteria in the indoor environment, study sample were collected indoor from 60 homes the sample were taken between 10:00 AM & 12:00 PM.

Samples was carried out using settle plates sedimentation technique, open Petri-dishes containing different culture media was employed to collect samples. Isolates were identified according to standard methods (Rajash and Rattan 2008). The settle plate method using 9 cm diameter Petri dishes. The sampling height was 1 m above the floor and at the center of the room. Bacteria were collected on nutrient and blood agar. To obtain the appropriate surface density for counting and to determine the load with respect to time of exposure, the sampling times were set at 60 min. After that the covers are replaced and plates were then incubated at 37° for 48 hours after which the colony forming units (CFU) were counted.

Once colony forming units (CFU) were enumerated, CFU/m^3 was estimated using Koch sedimentation method according to Polish Standard PN 89/Z-04008/08 (Bhatica L and Vishwakarma 2010)

$$CFU/M^3 = \frac{colonies\ on\ agar\ stripes}{sampling\ time\ in\ munites} \times 25$$

Bacterial colonies were initially characterized by morphology and microscopic examination and identified further by biochemical tests using "Biolgo Gen 111 microplate ™ " test panel which provides standardized micromethod using 94 biochemical test.

Data were analyzed by computer program. Descriptive statistics including percentage, mean and standard deviation were used for describing the bacterial count.

STATISTICAL ANALYSIS

All analysis was done using the statistical package for the social science (SPSS software version 22) on a personal computer.

RESULTS

We study airborne Bacteria in Indoor Environments in four residence areas covering summer, winter season to study the climate effect (temperature)

Table (1): Colony count and identification of bacterial samples(Air borne Bacteria) in summer season high level population.

Sample number	organism ID	No of Colony	CFU\m3
1	Exiguobacterium aurantiacum	24	10
	Dietzia maris	24	10
2	Exiguobacterium aurantiacum	27	11.25
	Dietzia maris	28	11.67
	Bacillus	30	12.5
3	Exiguobacterium aurantiacum	23	9.58
	Dietzia maris	24	10
	Staphylo coccus arlettae	24	10
4	Exiguobacterium aurantiacum	20	8.33
	Dietzia maris	34	14.17
	Staphylo coccus arlettae	21	8.75
5	Exiguobacterium aurantiacum	31	12.92
	Dietzia maris	30	12.5
6	Exiguobacterium aurantiacum	30	12.5
	Dietzia maris	31	12.92

Cont.Table(1): Colony count and identification of bacterial samples(Air borne Bacteria) in summer season high level population.

sample number	organism ID	No f Colony	CFU\m3
7	Exiguobacterium aurantiacum	25	10.42
	Paenibacillus ginsengarvi	27	11.25
8	Exiguobacterium aurantiacum	30	12.5
	Dietzia maris	35	14.58
	Bacillus	32	13.33
9	Exiguobacterium aurantiacum	22	9.17
	Dietzia maris	25	10.42
	Staphylo coccus arlettae	20	8.33
10	Exiguobacterium aurantiacum	29	12.08
	Dietzia maris	22	9.17
	Bacillus	32	13.33
11	Exiguobacterium aurantiacum	25	10.42
	Dietzia maris	31	12.92
	Paenibacillus ginsengarvi	30	12.5
12	Exiguobacterium aurantiacum	22	9.17
	Dietzia maris	25	10.42
13	Exiguobacterium aurantiacum	24	10
	Dietzia maris	20	8.33
	Staphylo coccus arlettae	23	9.58
14	Exiguobacterium aurantiacum	30	12.5
	Dietzia maris	19	7.92
	Bacillus	28	11.67
15	Exiguobacterium aurantiacum	23	9.58
	Dietzia maris	32	13.33
	Paenibacillus ginsengarvi	24	10

Table (2): Colony count and identification of bacterial samples (Air borne Bacteria) in winter season high level population.

sample number	organism ID	NO OF COLONY	CFU\m3
16	Bacillus	3	1.25
	Paenibacillus ginsengarvi	1	0.417
17	Staphylo coccus arlettae	3	1.25
	Dietzia maris	1	0.42
18	Bacillus	2	0.83
	Exiguobacterium aurantiacum	3	1.25
19	Staphylo coccus arlettae	3	1.25
	Dietzia maris	4	1.67
20	Bacillus	2	0.83
	Exiguobacterium aurantiacum	5	2.08
21	Staphylo coccus arlettae	5	2.08
	Dietzia maris	3	1.25
22	Bacillus	6	2.5
	Paenibacillus ginsengarvi	2	0.83
23	Bacillus	4	1.67
	Dietzia maris	5	2.08
24	Staphylo coccus arlettae	4	1.67
	Paenibacillus ginsengarvi	3	1.25
25	Staphylo coccus arlettae	3	1.25
	Exiguobacterium aurantiacum	3	1.25
26	Bacillus	2	0.83
	Exiguobacterium aurantiacum	2	0.83
27	Staphylo coccus arlettae	4	1.67
	Dietzia maris	5	2.08
28	Bacillus	6	2.5
	Exiguobacterium aurantiacum	3	1.25
29	Staphylo coccus arlettae	2	0.83
	Dietzia maris	3	1.25
30	Bacillus	6	2.5
	Exiguobacterium aurantiacum	3	1.25

Table(3): Colony count and identification of bacterial samples (Air borne Bacteria) in summer season low level population.

sample number	organism ID	No of Colony	CFU\m 3
31	Brachy bacterium conglomeratum	54	22.5
	Bacillus	56	23.33
32	Brachy bacterium conglomeratum	54	22.50
	Staphylo coccus arlettae	49	20.42
33	Brachy bacterium conglomeratum	52	21.67
	Bacillus	44	18.33
34	Brachy bacterium conglomeratum	52	21.67
	kytococcus aerolatus	54	22.50
35	Staphylo coccus arlettae	٤٤	١٨,٣٣
36	Brachy bacterium conglomeratum	42	17.5
	kytococcus aerolatus	48	20.00
37	Brachy bacterium conglomeratum	50	20.83
	kytococcus aerolatus	50	20.83
	Bacillus	55	22.92
38	Brachy bacterium conglomeratum	52	21.67
	kytococcus aerolatus	52	21.67
39	Brachy bacterium conglomeratum	55	22.92
	Staphylo coccus arlettae	56	23.33
40	Bacillus	52	21.67
	Brachy bacterium conglomeratum	60	25.00
41	Brachy bacterium conglomeratum	55	22.90
	kytococcus aerolatus	54	22.5
	Staphylo coccus arlettae	55	22.90
42	Brachy bacterium conglomeratum	59	24.6
	kytococcus aerolatus	52	21.67
	Bacillus	50	20.83
43	Brachy bacterium conglomeratum	48	20.00
	Staphylo coccus arlettae	48	20
	kytococcus aerolatus	54	22.5
44	Brachy bacterium conglomeratum	52	21.67
	kytococcus aerolatus	51	21.25
45	Brachy bacterium conglomeratum	52	21.70
	kytococcus aerolatus	56	23.30
	Staphylo coccus arlettae	53	22.1

Table (4): Colony count and identification of bacterial samples(Air borne Bacteria) in winter season low level population.

sample number	organism ID	No of Colony	CFU\m3
46	kytococcus aerolatus	7	2.92
	Bacillus	8	3.33
47	Brachy bacterium conglomeratum	11	4.58
	Staphylo coccus arlettae	10	4.17
48	Brachy bacterium conglomeratum	9	3.75
	kytococcus aerolatus	10	4.17
	Bacillus	8	3.33
49	kytococcus aerolatus	7	2.92
	Staphylo coccus arlettae	8	3.33
50	Brachy bacterium conglomeratum	7	2.92
	Staphylo coccus arlettae	9	3.75
51	Brachy bacterium conglomeratum	11	4.58
	kytococcus aerolatus	12	5
	Bacillus	15	6.25
52	kytococcus aerolatus	15	6.25
	Bacillus	10	4.17
53	Brachy bacterium conglomeratum	15	6.25
	kytococcus aerolatus	11	4.58
54	Staphylo coccus arlettae	15	6.25
55	kytococcus aerolatus	15	6.25
	Bacillus	13	5.42
56	kytococcus aerolatus	14	5.83
	Staphylo coccus arlettae	14	5.83
57	kytococcus aerolatus	13	5.42
	Staphylo coccus arlettae	12	5
58	kytococcus aerolatus	12	5
	Bacillus	12	5
59	Brachy bacterium conglomeratum	11	4.58
	Bacillus	10	4.17
60	Brachy bacterium conglomeratum	11	4.58
	Staphylo coccus arlettae	12	5

Table (5): Frequencies of airborne bacteria in High level residence during Summer season.

	Organism identification	Frequency	Percent %
1	Bacillus	4	10.0%
2	Dietzia maris	14	35.0%
3	Exiguobacterium aurantiacum	15	37.5%
4	Paenibacillus ginsengarvi	3	7.5%
5	Staphylococcus arlettae	4	10.0%

Table (6): Frequencies of airborne bacteria in High level residence during winter season.

	Organism identification	Frequency	Percent
1	Bacillus	8	26.7%
2	Dietzia maris	6	20.0%
3	Exiguobacterium aurantiacum	6	20.0%
4	Paenibacillus ginsengarvi	3	10.0%
5	Staphylococcus arlettae	7	23.3%

Table (7): Frequencies of airborne bacteria in Low level residence during Summer season.

	Organism identification	Frequency	Percent
1	Bacillus	4	12.1%
2	Brachybacterium conglomeratum	14	42.4%
3	kytococcus aerolatus	9	27.3%
4	Staphylococcus	6	18.2%
	Total	65	100.0%

Table(8): Frequencies of airborne bacteria in Low level residence during Winter season.

	Organism identification	Frequency	Percent
1	Bacillus	7	22.6%
2	Brachybacterium conglomeratum	7	22.6%
3	kytococcus aerolatus	10	32.2%
4	Staphylococcus	7	22.6%
	Total	65	100.0%

Table (9): Comparison of colony forming units of airborne bacteria during two seasons

Variable	CFU\m³			
	Minimum	**Maximum**	**Mean**	**Std. Deviation**
Summer high level	7.92	14.58	10.9687	1.82083
Winter high level	.42	2.50	1.3889	.59263
Summer low level	17.50	25.00	21.6913	1.64674
Winter low level	2.92	6.25	4.6640	1.06729
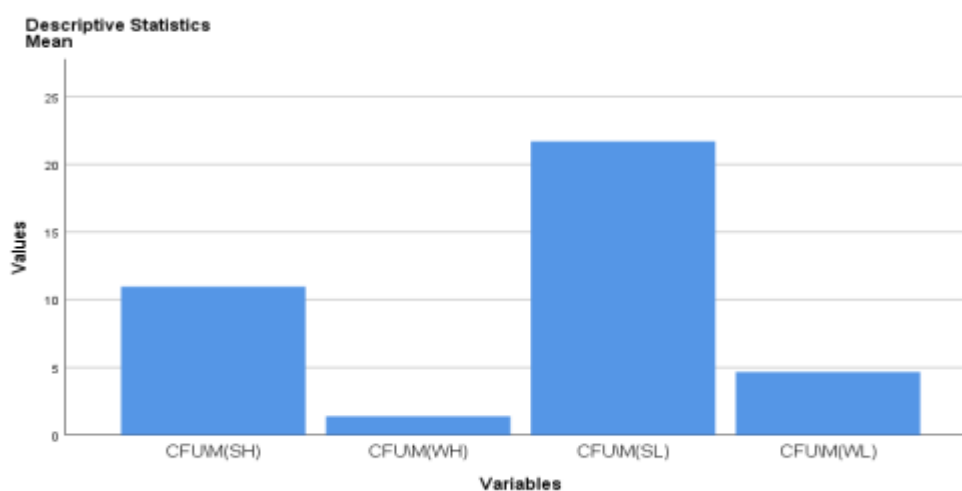
Figure (1): Comparison of colony forming units of airborne bacteria in the two levels.

* SH: high level population in summer, * WH: high level population in winter, *SL: low level population in summer, *WL: low level population in winter.

Table (10): Comparison of colony forming units of airborne bacteria among low level residence during two seasons.

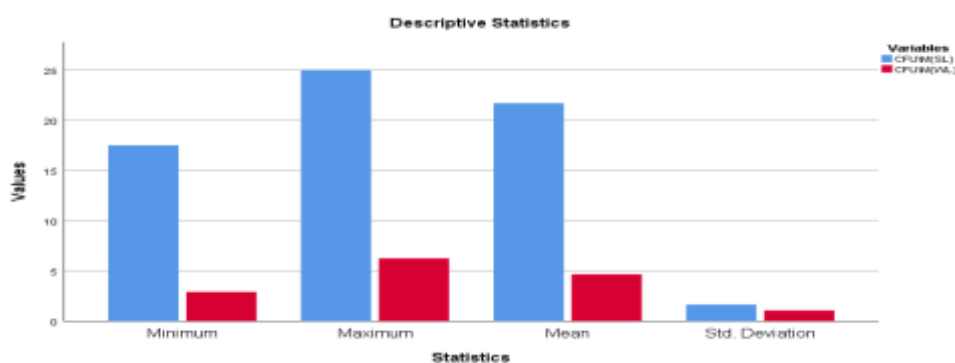| Season	CFU\m3			Std. Deviation	p-value
	Minimum	**Maximum**	**Mean**		
Summer season	17.50	25.00	21.6913	1.64674	P<0.001
Winter season	2.92	6.25	4.6640	1.06729	

Figure (2): Comparison of colony forming units of airborne bacteria among low level

residence during two seasons to study climate effect in airborne bacteria.

*SL : low level population in summer, *WL : low level population in winter

Table (11): Comparison of colony forming units of airborne bacteria among
High level residence during two seasons .

Season	CFU\m³			Std. Deviation	p-value
	Minimum	**Maximum**	**Mean**		
Winter season	0.42	2.50	1.3889	0.59263	
Summer season	7.92	14.58	10.9687	1.82083	P<0.001
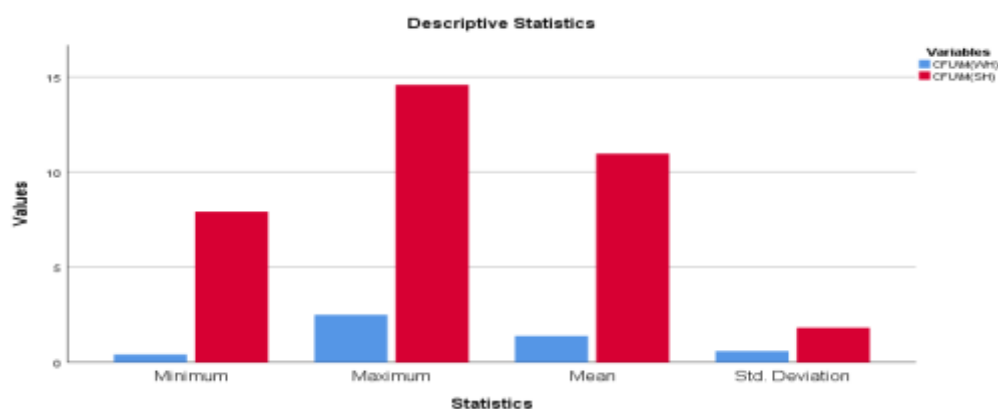
Figure (3): Comparison of colony forming units of airborne bacteria among

High level residence during two seasons.

* SH : high level population in summer, * WH : high level population in winter

Table (12): Comparison of colony forming units of airborne bacteria among high and low level residence during one summer season

Socioeconomic level	CFU/m3			Std. Deviation	p-value
	Minimum	**Maximum**	**Mean**		
low level	17.50	25.00	21.6913	1.64674	
High level	7.92	14.58	10.9687	1.82083	P<0.001
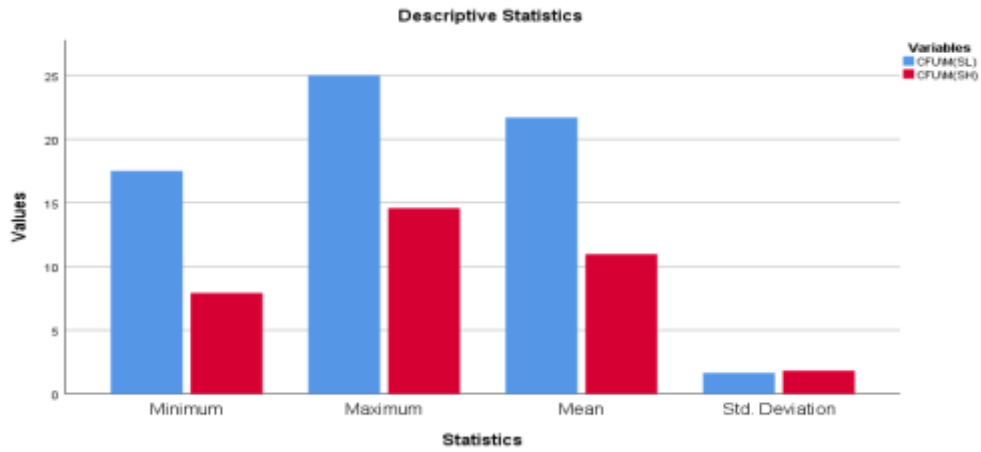
Figure (4): Comparison of colony forming units of airborne bacteria between high level residence and low level population during summer .

* SH : high level population in summer, *SL : low level population in summer,

Table (13): Comparison of colony forming units of airborne bacteria among high and low level residence during winter season

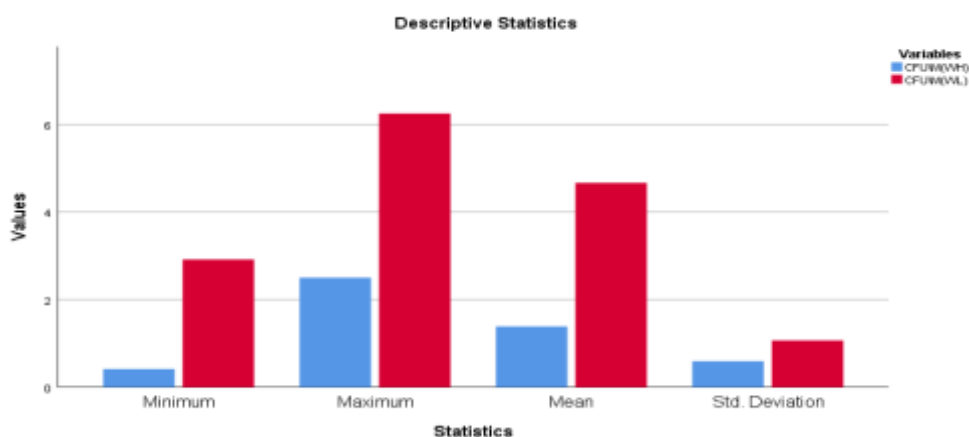| Socioeconomic level	CFU/m3			Std. Deviation	p-value
	Minimum	**Maximum**	**Mean**		
High level	.42	2.50	1.3889	0.59263	
low level	2.92	6.25	4.6640	1.06729	P<0.001

Figure (5): Comparison of colony forming units of airborne bacteria between high level residence and low level population during winter.

* WH : high level population in winter, *WL : low level population in winter

DISCUSSION

A review made by WHO on the number of epidemiological studies showed that, there is sufficient evidence for an association between indoor dampness-related factors and a wide range of effects on respiratory health, including asthma development, asthma exacerbation, current asthma, respiratory infections, upper respiratory tract symptoms, cough, wheeze and dyspnoea (WHO 2009) The activity of people and equipment within the indoor environments is thought to be the principal factor contributing to the buildup and spread of airborne microbial contamination(Hospodsky *et al*., 2012) Moreover, the environmental factors mainly include temperature, humidity, air exchange rate, air movement, building structures and location, poor design, ventilation system as well as interior or redesign which enhance microorganism's growth and multiplication in the indoor atmosphere.(Wamedo *et al*., 2012).

Tables 1, 2, 3 and 4 show colony count and identification of airborne bacteria in the two residence areas. Statistical analysis of these four tables shows that Exiguobacterium sp was the most frequent bacteria (37.5%) followed by Dietzia sp (35%), staphylococcus sp (10%), Bacillus sp (10%) and the less frequent Paenibacillus sp 7.5% among high level population during the Summer season (table 5). Bacillus sp was the most frequent bacteria (26.7%) followed by staphylococcus sp (23.3%), Exiguobacterium sp(20 %), Dietzia sp (20%) and the less frequent Paenibacillus sp(10%) among high level population during the Winter season (table 6). Brachybacterium sp was the most frequent bacteria (42.4%) followed by kytococcus spv(27.3%), staphylococcus sp (18.2 %) and the less frequent Bacillus sp (12.1%)in low level population in the summer climate(table 7).kytococcus sp was the most frequent bacteria (32.2%) followed by Brachybacterium sp, staphylococcus sp, Bacillus sp (22.6%)in low level population in the winter climate(table 8).

Colony forming unit was maximum in summer season low level population (table 9) which indicate high level of airborne bacteria due to high temperature and low quality of life as shown in Fig 1.

A significant increase in colony forming unit in low level residence population in summer with Minimum, Maximum, Mean value 17.5, 25, 21.69 CFU/m3 respectively than in low level residence population in winter with Minimum, Maximum, Mean value 2.92, 6.25, 4.66 CFU/m3 respectively with p-value <0.001(table 10) which indicate high level of airborne bacteria due to high temperature as shown in Fig 2.

A significant increase in colony forming unit in high level residence population in summer with Minimum, Maximum, Mean value 7.92, 14.58, 10.69

CFU/m3 respectively than in high level residence population in winter with Minimum, Maximum, Mean value 0.42, 2.5, 1.39 CFU/m3 respectively with p-value <0.001(table 11) which indicate high level of airborne bacteria due to change in temperature as shown in Fig 3.

A significant increase in colony forming unit in low level residence population in summer with Minimum, Maximum, Mean value 17.5, 25, 21.69 CFU/m3 respectively than in high level residence population during summer with Minimum, Maximum, Mean value 7.92, 14.58, 10.97 CFU/m3 respectively with p-value <0.001(table 12) which indicate high level of airborne bacteria due to low ventilation and cleaning facilities as shown in Fig 4.

A significant increase in colony forming unit in low level residence population during winter with Minimum, Maximum, Mean value 2.92, 6.25, 4.66 CFU/m3 respectively than in High level residence population in winter with Minimum, Maximum, Mean value 0.42, 2.5, 1.39 CFU/m3 respectively with p-value <0.001(table 13) which indicate high level of airborne bacteria due to low ventilation and cleaning facilities as shown in Fig 5..

The concentrations of bacteria measured in all sites were significantly different to each other (P-value <0.001). These can be mainly explained by the variation of density of occupant during sampling time in low level population as well as the variation of ventilation conditions and climate changes

CONCLUSION& RECOMMENDATION

According to statistical study of samples in the two levels there were significant differences in bacterial growth which reflect the effect of socioeconomical quality of life and also reflects the effect of climate (temperature) change in bacterial growth in indoor environment. Thus:

1. Attention must be given to control environmental factors which favor the growth and multiplication of microbes in indoor environment.

2. Further studies must be done to asses health effect on human due to indoor air pollution by airborne bacteria.

3. Increasing health education to socioeconomic low level population.

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دراسة الكائنات الحية الدقيقة داخل بيئة المسكن

[٣]

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المستخلص

البكتيريا موجودة تقريبا في كل بيئة. المستويات عالية من تركيز البكتيريا في الداخل هو مؤشر على ارتفاع معدل الإشغال، وسوء التهوية، أو سوء صيانة المباني. ندرس البكتريا المنقولة بالهواء في البيئات الداخلية في منطقتين سكنيتين تغطي فصل الصيف، فصل الشتاء لدراسة تأثير المناخ (درجة الحرارة) كما تغطي مستوى معيشي عالي ومستوى معيشي منخفض من السكان لدراسة تأثير جودة الحياة (التهوية الجيدة والتهوية وتغيير المساحة المتاحة لكل مواطن) في التلوث بالبكتريا في الأماكن المغلقة. ندرس وجود البكتيريا المحمولة جواً في البيئات الداخلية ووحدة تشكيل المستعمرات لكل حالة ووجدنا أن Heliobacterium sp هي أكثر أنواع البكتيريا شيوعًا (37.5%) في التجمعات السكانية ذات المستوى المعيشي العالي الصيفي، وكان Bacillus sp الأكثر شيوعًا البكتيريا (٢٦,٧ ٪) في التجمعات السكانية ذات المستوى المعيشي العالي في مناخ الشتاء، Brachybacterium كانت البكتيريا الأكثر شيوعا (٤٢,٤ ٪) في التجمعات السكانية ذات المستوى المعيشي المنخفض في المناخ الصيفي وكان kytococcus الأكثر البكتيريا شيوعا (٣٢,٢ ٪) في التجمعات السكانية ذات المستوى المعيشي المنخفض في مناخ الشتاء. وجدنا زيادة ملحوظة في وحدة تشكيل المستعمرات في التجمعات السكانية

ذات المستوى المعيشي المنخفض في المناخ الصيفي مع الحد الأدنى، الحد الأقصى، القيمة المتوسطة ١٧,٥، ٢٥، ٢١,٦٩ وحدة تكوين مستعمرة/مل على التوالي مقارنة بالتجمعات السكانية ذات المستوى المعيشي العالي في مناخ الصيف مع الحد الأدنى، الحد الأقصى، القيمة المتوسطة ٧,٩٢، ١٤,٥٨، ١٠,٩٧ وحدة تكوين مستعمرة/مل على التوالي مع القيمة الاحتمالية ١٠٠٠,٠> التي تشير إلى التأثير السلبي لمعدل الإشغال المرتفع، والتهوية السيئة على جودة الحياة وزيادة كبيرة في وحدة تشكيل المستعمرة في السكان المقيمين على مستوى عال في الصيف مع الحد الأدنى، والحد الأقصى، والقيمة المتوسطة ٧,٩٢، ١٤,٥٨، ١٠,٦٩ وحدة تكوين مستعمرة/مل على التوالي مقارنة بالسكان ذوي المستوى العالي في الشتاء مع الحد الأدنى، الحد الأقصى، القيمة المتوسطة ٠,٤٢، ٢,٥، ١,٣٩ وحدة تكوين مستعمرة/مل على التوالي مع القيمة الاحتمالية ٠,٠٠١> .٠ والتي تشير إلى مستوى عال من البكتيريا المحمولة جوًا بسبب ارتفاع درجة الحرارة .